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(54) TNF receptor action modulation.

(57) A method of modulating signal transduction and/or cleavage in Tumor Necrosis Factor Receptors (TNF-Rs) is provided. Peptides or other molecules may interact either with the receptor itself, or with effector proteins interacting with the receptor, thus modulating the normal functioning of the TNF-Rs. Such peptides or other molecules may be employed for prophylactic and therapeutic applications in TNF associated diseases.

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The present invention relates to the modulation of signal transduction by the tumor necrosis factor receptors (TNF-Rs) and to modulation of the cleavage of these TNF-Rs. More particularly, the invention provides peptides and other substances which interact either with the TNF-Rs, or with effector proteins interacting with the receptor, and thus can be employed for prophylactic and therapeutic applications in diseases associated with the function of TNF.

TNF, a pro-inflammatory cytokine produced primarily by macrophages, contributes to the defense of the host against pathogens as well as to various detrimental manifestations of inflammation through a variety of different effects on cell function (Old, 1990; Beutler and Cerami, 1989). These effects are initiated by the binding of TNF to specific, high affinity cell surface receptors (TNF-Rs), expressed on most kinds of cells (Baglioni et al., 1985; Beutler et al., 1985; Kull et al., 1985; Tsujimoto et al., 1985; Aggarwal et al., 1985; Israel et al., 1986). The receptors provide the intracellular signals for cell response to TNF (Engelmann et al., 1990a). Two molecular species of the TNF-Rs, the P55 and the p75 TNF-R, expressed differentially in different types of cells, have been identified (Engelmann et al., 1990b; Brockhaus et al., 1990).

One of the most distinct characteristics of TNF compared to other immune system mediators is its ability to elicit cell death. In many severe diseases, such as autoimmune disorders, rheumatoid arthritis, graft rejection and graft-versus-host disease, TNF seems to be a major cause for pathological tissue destruction. Blocking TNF activity in these conditions is therefore of the highest importance for the development of new therapies for these diseases.

On the other hand, in certain other situations it is advantageous to augment the function of TNF, e.g. in situations where its anti-tumor or antibacterial activities are beneficial.

The main mediator for the cytotoxic effect of TNF on fibroblastoid and epithelial cells is the p55 TNF-R, which also is the prevalent TNF-R type on these cell lines. Blocking this receptor species abolishes the cytocidal effect of TNF, while inducing aggregation of the receptor molecules can mimic the cytocidal effect of TNF.

The soluble form of this receptor, as well as the soluble form of the other (p75) TNF-R, have been shown to have inhibitory effects on TNF function. Evidence was presented that these soluble forms are derived proteolytically from the cell surface forms, (Nophar et al., 1990; Porteu and Nathan, 1990; Porteu et al., 1991).

Both the signaling by the receptors and the cleavage of the receptors appear to reflect interactions between the receptor and some cellular effector proteins; the cleavage - by interacting with regulatable proteases, and the signaling - by interacting with proteins having some signaling activity.

The present invention provides a method of modulating signal transduction and/or cleavage in tumor necrosis factor receptors (TNF-Rs) comprising interfering with one or more amino acids in the sequence of a TNF-R or with an effector protein interacting with the TNF-R.

This interference influences the normal functioning of the TNF-Rs or influences an effector protein interacting therewith, and thereby modulates signal transduction by causing partial or total inhibition thereof, or influences shedding, i.e. abolishes cleavage of the soluble form of the receptor.

The present invention further provides peptides or other molecules which interact either with the receptor itself, i.e. interact with one or more amino acids in the receptor sequence, or interact with the effector proteins, and thus modulate the normal functioning of the TNF-Rs. The above molecules also include antibodies or fragments thereof.

The peptides and other substances may either be produced by conventional or by recombinant methods.

The invention also provides pharmaceutical compositions comprising the above peptides or other substances for treatment of TNF related disorders.

Figure 1 shows the nucleotide and amino acid sequences of the p55 TNF receptor therein the circled portions are the sequences of the leader and transmembrane domains and the arrows denote the mutations and deletions performed.

Figure 2 illustrates various deletion mutants examined.

Figure 3 demonstrates that the mutant of the P55 TNF-R in which amino acids 415-426 were deleted can still signal for a cytocidal effect while the mutant Δ:405-426, from which additional 10 amino acids were deleted, cannot.

Figure 4 shows that a mutant of p55 TNF-R in which 197 ser was replaced by ala has decreased ability to transduce the signal for the cytocidal effect.

Figure 5 demonstrates that the mutation in which 197 ser was replaced by ala abolishes the inducible shedding of the extracellular part of the p55 TNF-R.

Figure 6 demonstrates that deletion of either amino acids 170-174 or 175-179, as well as deletion of all amino acids 170-179 abolishes the inducible shedding of the extracellular portion of the p55 TNF-R.

A short stretch of amino acids in the intracellular part of the p55 TNF receptor was identified, which was found to be essential for the triggering of cell death by TNF. Mutants of the p55 TNF-R

with C-terminal deletions in the intracellular part cannot signal for the cytotoxic effect, if this stretch of amino acids was deleted. In contrast, truncated receptors containing this amino acid sequence are fully able to elicit cell death. Molecules which can specifically bind to this sequence as well as molecules which mimic the structure of this sequence but lack its ability to stimulate cell death, can be applied as intracellular inhibitors against TNF. They will inhibit the interaction of the TNF-Rs with molecules functioning downstream in the signal transduction chain.

Moreover, a specific amino acid in the transmembrane domain of the human p55 TNF-R was identified, which is necessary to trigger the full cytotoxic effect of TNF and also plays a decisive role in the shedding of the soluble form of the receptor. Exchange of this amino acid with a "neutral" amino acid severely impairs the signaling, yet does not lead to complete inactivation of the signal transduction mechanism. It also abolishes shedding of the soluble form of the receptor. Therefore, molecules which are designed to specifically interact with this amino acid can attenuate the cytocidal activity of TNF as well as making available more receptor sites on the surface of the cells due to the inhibition of the shedding of the extra-cellular, soluble form of the receptor, and thus will allow the use of TNF for therapeutic purposes without eliciting cell death.

Another stretch of amino acids in the region of the receptor just external to the transmembrane region was also found to be essential for cleavage of the soluble form of the receptor. Therefore, interference with this stretch, or with effector proteins interacting therewith, will also influence the functioning of the receptor.

Clones of A9 cells expressing wild type and mutant forms of the human p55 TNF-R were identified by binding of radiolabelled human TNF. Clones exhibiting approximately ten-fold enhancement of TNF binding compared to non-transfected or control-transfected, i.e. transfected only with the neomycin resistance conferring plasmid, A9 cells, were employed for further work.

Probing the sensitivity of the transfected cells to the cytocidal effect of TNF with monoclonal antibodies against the human p55 TNF-R, which can mimic TNF action, different effects in transfectants with wild type or mutant receptors were observed. Cells transfected with the wild type human p55 TNF-R became highly sensitive to the cytotoxic action of these antibodies, which showed no effect on untransfected or control-transfected A9 cells. In contrast, transfectants expressing mutant receptors with deletion of the intracellular amino acids 405 to 426 were absolutely not responsive to antibodies against the human p55 TNF-R, in spite of similar levels of receptor expression. Still, these cells could respond to human TNF acting via the endogenous murine receptors for TNF, proving that the insensitivity was not due to a post-receptor blockade in the signal transduction pathway.

Receptor mutants (del:415-426), with a deletion 10 amino acids shorter than in the aforementioned mutant, however, conferred to the transfected cells high responsiveness to the cytocidal action of antibodies against the human p55 TNF-R.

The above shows that amino acids 405 to 414, or part of them, are essential for the signaling of the human p55 TNF-R for the cytotoxic effect of TNF, whereas amino acids 415 to 426 are not essential.

In a third nutant, a single serine residue (amino acid 197) in the transmembrane domain was exchanged by site directed mutagenesis against alanine, an amino acid said to be compatible with all known secondary structures of amino acid sequences. Funtional analysis of cells transfected with this receptor mutant revealed a significant impairment in these receptors to trigger cell death in response to mimetic antibodies against the human p55 TNF-R. Yet this functional disruption was not complete and a small cytocidal effect could still be observed.

Yet other mutants, in which either amino acids 170-174, 175-179 or both, i.e., amino acids 170-179, were deleted, abolished shedding of the soluble extracellular forms of the receptor. This finding demonstrates that the region of amino acids 170-179 or part thereof, of the receptor, which lies just outside the transmembrane domain, must be intact in order to allow formation of the soluble TNF receptors. Therefore, any interference with this region, or the effector protein interacting therewith, will abolish shedding. The effector protein, in this case, is believed to be a proteolytic enzyme.

As stated above, the present invention provides, amongst others, peptides and other molecules which can interact either with the receptor itself, or a certain region thereof, or with effector proteins interacting with the receptor, and to methods for the production of these peptides and substances.

For this purpose, proteins which interact with the relevant regions of the receptor are isolated from cellular extracts, e.g. by ligand affinity purification using these regions as ligands. Thereafter screening is carried out for substances which bind either with the receptor or with those isolated effector proteins, thus interfering with their interaction with each other. Such screening is effected in any one of the following ways:

1) Target peptides which correspond to the amino acid regions of the TNF-R found to be critical for signal transduction and/or shedding are syn-

thesized and peptide libraries are screened for ligands which bind thereto. The peptides which bind to these regions are further screened for those which also bind to TNF-R. Finally, the peptides capable of high affinity binding with both the target peptides and the TNF-R, are screened for the ability of the peptide to perform the desired biological activity, i.e. influence the normal functioning of TNF-R.

2) In a similar manner, a variety of organic molecules, including drugs known for other indications, are screened for their ability to interfere with the normal functioning of TNF-R. This is determined by examining whether these molecules can bind or interact in a different manner with the amino acids or amino acid regions found to be critical for signal transduction and/or shedding of the TNF-R.

3) In addition to the organic molecules, also broth of biological matter, such as bacteria culture products, fungi culture products, eukaryotic culture products and crude cytokine preparations are screened with the amino acid target peptides described above. Molecules obtained by this screening are then further screened for their ability to perform the desired biological function.

In the same manner, effector proteins obtained, e.g. by chromatography of all extracts through a resin to which the target peptides were linked, are employed for screening of the above peptide libraries, organic molecules and biological broths. The molecules found in this manner to bind to the effector proteins are then examined for their ability to inhibit the interaction between the effector proteins and the TNF-R and thus for their ability to interfere with the normal functioning of the TNF-R.

Alternatively, molecules are designed which spatially fit the quaternary structure of the amino acid regions in the receptor or the effector protein, and thus interfere with the interaction of the two.

The active molecules obtained by the above procedures, inasfar as they are biological substances, can also be prepared by biotechnological approaches. In this way, massive production of these molecules will be made possible. Peptides may either be produced by known peptide synthesis methods or using expression vectors containing DNA sequences encoding them. Other molecules, if produced in an enzymatic way, can be made by producing the enzymes involved in the appropriate cultured cells.

Pharmaceutical compositions containing the peptides or other molecules of the present invention may be employed for either antagonizing the deleterious effect of TNF in mammals, i.e. for treating conditions where excess TNF is either endogenously formed or exogenously administered, or for augmenting the beneficial effects of TNF, i.e. in the treatment of tumors.

Such compositions comprise the active peptides or other molecules according to the invention as their active ingredient. The pharmaceutical compositions are indicated for any conditions of excess TNF, such as in septic shock, cachexia, graft-versus-host reactions, autoimmune diseases such as rheumatoid arthritis, and the like. They are also indicated for counteracting e.g. an overdose of exogenously administered TNF.

The pharmaceutical compositions according to the invention are administered depending on the condition to be treated, via the accepted ways of administration. For example, in the case of septic shock, intravenous administration will be preferred, while in the case of arthritis, local injection may be indicated. The pharmaceutical compositions may also be administered continuously, i.e. by way of infusion, or orally. The formulation and dose will depend on the condition to be treated, the route of administration and the condition and the body weight of the patient to be treated. The exact dose will be determined by the attending physician.

The pharmaceutical compositions according to the invention are prepared in the usual manner, for example by mixing the active ingredient with pharmaceutically and physiologically acceptable carriers and/or stabilizers and/or excipients, as the case may be, and are prepared in dosage form, e.g. by lyophilization in dosage vials.

The following examples illustrate the invention without limiting it thereto:

Example 1: Construction of mutant p55 TNF receptors

The cDNA of the human p55 TNF-R (Nophar et al., 1990) was digested with the BanII and NheI restriction enzymes, resulting in removal of large parts of the 5, and 3' non-coding regions. Mutants Δ:405-426 and Δ:415-426 (Fig. 3) were generated by oligonucleotide directed mutation of this shortened form of the cDNA, using the "Altered Sites" mutagenesis kit of Promega. Stop codons were introduced after cysteine 404 (mutant Δ:405-426; amino acids in the receptor are numbered according to Loetscher et al., 1990), using the oligonucleotide 5'CTG CTG GGC TGC TAG CCT GGA GGA CAT 3', and after glycine 414 (mutant Δ:416-426), using the oligonucleotide 5'AAG CCC TTT GCG GCT AGC CCC GCC GCC CT 3'. Other mutants of the cDNA were produced similarly using the appropriate oligonucleotides to direct the desired mutations for the remaining mutants examined. The wild type and mutated cDNAs were introduced into the eukaryotic expression vector

pMPSVEH (Artelt et al., 1988), which contains the myeloproliferative sarcoma virus promoter, an SV40 intron and the SV40 polyadenylation signal.

Example 2: Expression of the wild type and the mutant receptors in cultured cells

Cells of the murine A9 line were cultured with Dulbecco's modified Eagle's Medium (DMEM), containing 10% fetal calf serum, 100 units/ml penicillin and 100 µg/ml streptomycin (growth medium). The cells were transfected with the expression constructs encoding the wild type and the mutant receptors, together with the neomycin resistance-conferring plasmid pSV2neo, using the calcium phosphate precipitation method (Graham and van der Eb, 1973). After 10 to 14 days selection in growth medium containing 500 µg/ml G418 (Sigma), resistant colonies were isolated and examined or expression of the human p55 TNF-R (hu-p55-TNF-R) by measuring TNF binding to the cells. Of all transfectants at least three different clones were analysed in the functional assays to check for clone-to-clone variations of their properties.

Example 3: Determination of TNF binding to cells

Recombinant human TNF-α (TNF, $6X10^7$ units/mg of protein), produced by Genentech Co., San Francisco, CA, was kindly provided by Dr. G. Adolf of the Boehringer Institute, Vienna, Austria. The TNF was radiolabelled with chloramine T to a specific radioactivity of 2000 mCi/mmol (Israel et al., 1986). To determine the binding of TNF, cells were seeded into 15 mm tissue culture plates at a density of $2.5X10^5$ cells/plate. After 24 hr incubation at 37°C, the plates were transferred to ice, the growth medium was removed and radiolabelled TNF was applied at a concentration of 0.1 nM, either alone or witha 1000-fold excess of unabelled TNF, in 200 µl PBS (0.154 sodium chloride plus 10 mM sodium phosphate, pH 7.4) containing 1 mM $CaCl_2$, 1 mM $MgCl_2$, 0.5% BSA and 0.02% NaN_3 - (binding buffer). After 3 hr of incubation on ice, the cells were rinsed and then detached by incubation in PBS containing 5mM EDTA. Cell-bound radioactivity was determined in a gamma-counter.

Example 4: Quantification of the cytocidal efect of TNF and of antibodies to the hu-p55-TNF-R

Cells were seeded into 96 well plates, 24 hr before the assay at a density of 30,000 cells per well. The growth medium was then exchanged with 100 µl growth medium containing cycloheximide (CHI, 25 µg/ml for the HeLa cells and 50 µg/ml for all other cell types) and human TNF-α or monoclonal antibodies against the human p55 TNF-R (Engelmann et al., 1990b). After further 11 hours of incubation at 37°C, viability of the cells was assessed in a neutral red uptake assay as described before (Wallach, 1984).

Example 5: Isolation of effector proteins by ligand affinity purification

Synthetic peptides whose sequences correspond to those regions in the receptors found critical for signaling or cleavage are linked to a solid resin, e.g. Sepharose, Agarose or acrylamide hydrazide agarose or the like, by a covalent linker such as glutaraldehyde. Extracts of cells or cell membranes are applied to such a column and proteins binding to them eluted, e.g. by reduction of the pH. The fractions containing the proteins are collected and further purified according to conventional methods. The protein may be further purified. In this further purification, the proteins can be followed by determination of their specific activity (proteolytic or signaling).

Example 6: Preparation of antibodies or fragments thereof which interact with the TNF-R or with the effector proteins

The TNF-R or regions in it found to be critical for its function, or purified effector proteins interacting with them are injected into mice, rabbits or other suitable animals commonly used for development of antibodies using appropriate protocols. Monoclonal antibodies are developed against the above proteins using spleens of the immunized animals in the usual manner. DNA extracted from the spleen cells or from hybridomas developed therefrom are used to produce the antibodies by recombinant DNA technologies. In this manner, antibodies which modulate the function of TNF, either by interfering with its signal transduotion or with the cleavage of the receptor, are obtained.

Using the DNA which encodes the antibodies, smaller molecules with the same binding activity whose structure corresponds to the hypervariable regions in the antibodies and derivatives thereof, are constructed. These molecules are designed in a manner which allows them also to penetrate the cell membrances in order to interact with the cytoplasmic domain of the receptors or with cytoplasmic effector proteins.

Example 7: Identification of organic molecules or of other components of biological broths which interfere with receptor-effector proteins interactions

Effector proteins isolated and purified as in example 5 are labelled e.g. with ^{125}I or another radioactive tracer or with a fluorescent marker, and the effectivity of their interaction with solid phase bound receptor molecules or fragments thereof is measured in the presence of various biological broths or synthetic organic molecules in order to identify a molecule or molecules, which are capable of inferering with this interaction. By the same method such molecules can be followed in their purification from the crude preparations.

Example 8: Preparation of a peptide capable of interfering with the function of TNF-R (signal transduction or shedding)

A. Synthesis of target peptides

The target peptides have the following sequences:

Peptide A: Ile Glu Asn Val Lys

Peptide B: Gly Thr Gln Asp Ser

Peptide C: Ile Glu Asn Val Lys Gly Thr Gin Asp Ser

Peptide D: Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly

Peptide A corresponds to amino acids 170-174, peptide B to amino acids 175-179, peptide C to amino acids 170-189, and peptide D to amino acids 405-414 of the amino acid sequence of TNF-R as shown in Fig. 1.

The target peptides are synthesized using Fmoc protected amino acid derivatives, according to the usual procedures, e.g. according to Chang, C.D., and Meienhoffer, J., (1978); Grandas, A., et. al. (1989); Fournier, A., et. al. (1989); Stewart M.J. and Young J.D., (1984); or similar methods.

B. Synthesis of combinatorial peptide library Beads and linkers

The combinatorial peptide library is synthesized on suitable bead carriers, e.g. beads made of polystyrene crossed with divinyl benzene (1% DVB), diameter about 200 microns, containing about 1 mili-equivalent of binding site, e.g. primary amines, or acid labile chloromethyl group. Linkers, such as cystamine, can be coupled to the beads by using a suitable cross linker e.g. glutardialdehyde. Peptide synthesis is performed on the free amine of the cystamine. At the termination of the synthesis, the cystamine bridge is cleaved by mild reduction, e.g. by use of dithiotreitol, resulting in a peptide having a free C terminal SH group. This group, which in many peptides is unique, serves as a specific modification site for binding of a recognition molecule, e.g. by reaction with iminobiotin-maleimide.

Library Synthesis strategy

Primary library

The library synthesis strategy is designed to allow screening of peptides of sizes of 9 or more residues, and composed of up to about 100 different amino acid derivatives. The first 6 amino acids are randomly synthesized by incorporation of all the different amino acid derivatives into each synthesis cycle. In the last 3 synthesis cycles, a unique sequence of amino acids per bead is synthesized, as follows:
Following the incorporation of amino acid no. 6, the beads are aliquoted. The number of aliquots is identical to the number of different amino acid derivatives. A single amino acid derivative is then incorporated into the 7th position of growing polypeptide chain of all the beads in a single aliquot. The beads are then mixed together, and redistributed as before. This procedure is repeated 3 times, resulting in incorporation of a total of 3 unique amino acid residues per bead. This format of synthesis is called "structured synthesis" to differentiate from the random synthesis format used to synthesize the peptide in positions 1-6.

The primary library is then screened as described below. The results of the screening allow selection of specific tripeptide sequences capable of binding to the target sequences.

Secondary library

Synthesis of the secondary library is performed after the appropriate tripeptide sequence(s) are identified by screening of the primary library. The synthesis of the secondary library is carried out similarly to the synthesis of the primary library in concept. The first 3 amino acid residues are randomly synthesized, the next 3 amino acid residues are synthesized by structured synthesis, and the last 3 amino acids are synthesized according to the sequence(s) derived from screening of the primary library.

Tertiary library

The tertiary library is synthesized similarly to the primary and secondary libraries in concept. The first 3 amino acid residues are synthesized by structured synthesis, and the final 6 amino acid residues are incorporated according to the sequence(s) derived from screening of the primary and secondary libraries.

C. Extended synthesis/screening process

The process described above results in identification of peptides composed of 9 amino acid residues, which are capable of binding specifically to the target ligands. It is possible to continue the synthesis/screening process in order to prepare longer peptides, which might perform better. It may also be advantageous to further modify the peptide, e.g. stabilize the peptide conformation by cross-linking of side chains, protect against proteolytic cleavage by modification of the peptide bond, increase potential for transmembrane transport by conjugation of hydrophobic residues to side chains, etc., in order to improve its activity. It is then possible to carry out the modifications according to the above strategy. This approach allows fast screening of many modified peptides and greatly reduces the time needed in order to identify the desired peptide.

D. Screening of the library

The screening of the library (peptides) is divided into 2 phases:
Phase A: Screening for ligand binding i.e. binding to the target peptide and to the native protein.
Phase B: Screening for the capability of the peptides to diminish or abolish TNF-R shedding in response to TNF, or to block signal transduction by the TNF-R.

Phase A: Screening for ligand binding potential

The libraries are exposed to the ligand, e.g. any of the target peptides indicated above or the purified TNF-R. Detection of the bound ligand is possible following direct labeling of the ligand, e.g. by labeling with a fluorescent dye, such as tetramethyl rhodamine, or by using specific polyclonal antibodies and an appropriate second antibody coupled to a suitable marker, e.g. the enzyme alkaline phosphatase or horseradish peroxidase. The bound enzyme is detected using an appropriate substrate e.g. for alkaline phosphatase BCIP coupled with a tetrazolium salt such as nitroblue tetrazolium, or for horseradish peroxidase chloronaphtol or tetramethyl benzidine.

Detection of beads which bind the ligand is effected either by monitoring bead fluorescence e.g. by using a FACS machine, or by monitoring bead color by visual inspection. The labeled beads are retrieved from the mixture and the peptides of individual beads are sequenced by automatic peptide sequencer. The sequence data obtained enable designing of further libraries.

After detection of beads which bind to the target peptide, their binding to the protein carrying the target peptide is confirmed. This is carried out using a process similar to the one used for determination of the binding of the target peptide, but using highly purified TNF-R as ligand.

Phase B: screening for bioactivity

After identification of peptides capable of high affinity binding with the target peptides and to the TNF-R through the library screening cycles described above has been effected, screening for the ability of the peptide to perform the desired biological activity is carried out. Here we distinguish between peptides which are expected to operate outside of the cell (the peptide intended to block the TNF-R shedding) and peptides which are intended to operate inside the cytoplasm, such as those intended to block the signal transduction by the TNF-R.

Example 9: Screening for pentides intended for elimination of TNF-R shedding

All peptides capable of binding to the target peptides A, B or C and to the extracellular domain of the TNF-R are tested for their ability to reduce shedding of the TNF-R in response to TNF.

Cells are reacted with a mixture of peptides capable of binding to the extracellular domain of the TNF-R. Following incubation, the cells are lysed and the TNF-R molecules are purified by immunoaffinity on an appropriate McAb. It is assumed that only those TNF-R molecules would remain at the cell surface whose shedding was prevented by the respective peptides. Thus, the purified TNF-R molecules are expected to carry those inhibiting peptides. The peptides are purified from the purified TNF-R preparation, and sequenced. Alternatively, the desired peptides are eluted directly from the cells themselves, obviating the need to purify the TNF-R. Since the TNF-R is shed from the cells by cleavage at a site which is very close to the cell membrane, it is expected that all the peptides which bind at sites distant from the cleavage site would be removed from the cell surface together with the shed TNF-R segment. The peptides extracted from the cells are purified by SEC-HPLC or alternatively the peptides are labeled with iminobiotin (as described above) and purified by affinity chromatography using avidin columns.

Example 10: Screening of peptides intended for inhibition of signal transduction by the TNF-R

Screening for peptides capable of inhibiting signal transduction by the TNF-R is bore complicated. The major obstacle for the ability of the peptides to interfere with the signal transducing capability of the TNF-R, is their need to cross the cell membrane and accumulate in high enough concentration in the cytoplasm of the target cell.

The screening therefore has to be divided. In the initial screening, performed as described above, peptides are tested for the ability of the peptides (on beads) to bind to the target peptides and to the purified intracellular domain of the TNF-R molecule. Those peptides capable of binding are screened for their ability to block the signal transduction by the TNF-R. In order to facilitate the transport of the peptide through the membrane and into the cytoplasm, the peptides are chemically modifed on the beads e.g. (1) by oxidation of methionine to sulfoxide, (2) by replacing the peptide bond with its ketomethylene isoester ($COCH_2$) (Zacharia S., et. al. (1991)); (3) by introduction of lauroyl derivatives (Muranishi et. al. (1991)).

Modification of the peptides is carried out when the peptides are on the beads. The modified peptides are screened for their ability to bind to the intracellular domain of the TNF-R. Those peptides which retain the ability to bind to the TNF-R are cleaved from the beads and are further tested using live cells expressing the TNF-R for their ability to pass the membrane and block the TNF-R signal transduction.

Example 11: Creation of inhibitors of signaling and cleavage which spatially fit the regions of the TNF-Rs found critical for function

The 3-dimensional structure of the TNF-R is determined by X-Ray crystallography of crystals produced thereof. Special attention must be given to the structure of the regions found by the mutation analysis (figs. 3 to 6) to be critical for the signaling or cleavage of the receptor. Three-dimensional structures of known molecules are compared to the structures conceived by the above analysis in order to complement the structure of those critical regions. Molecules found in this way to resemble the derived complementary structure are examined for their ability to interfere with the signaling or cleavage of the receptors. If found to have any sign for effect, these molecules are modified by creating derivatives thereof in order to further approach the desired complementary structures. In such sequential modification of the structure and determination of bioactivity, effective inhibitors of signaling and proteolysis are obtained.

Example 12: Creation of recombinant DNA molecules comprising nucleotide sequences coding for the active peptides and other molecules and their expression

The peptides and other molecules can also be prepared by genetic engineering techniques and their preparation encompasses all the tools used in these techniques. Thus DNA molecules are provided which comprise the nucleotide sequence coding for such peptides and other biological molecules. These DNA molecules can be genomic DNA, cDNA, synthetic DNA and a combination thereof.

Creation of DNA molecules coding for such peptides and molecules is carried out by conventional means, once the amino acid sequence of these peptides and other molecules has been determined.

Expression of the recombinant proteins can be effected in eukaryotic cells, bacteria or yeasts, using the appropriate expression vectors. Any method known in the art may be employed.

For example, the DNA molecules coding for the peptides or other molecules obtained by the above methods are inserted into appropriately constructed expression vectors by techniques well known in the art (see Maniatis et al., (1982)). Double-stranded cDNA is linked to plasmid vectors by homopolymeric tailing or by restriction linking involving the use of synthetic DNA linkers or blunt-ended ligation techniques. DNA ligases are used to ligate the DNA molecules and undesirable joining is avoided by treatment with alkaline phosphatase.

In order to be capable of expressing a desired biological substance, i.e. a peptide or protein (hereinafter "protein", for simplicity's sake), an expression vector should comprise also specific nucleotide sequences containing transcriptional and translational regulatory information linked to the DNA coding for the desired protein in such a way as to permit gene expression and production of the protein. First, in order for the gene to be transcribed, it must be preceded by a promoter recognizable by RNA polymerase, to which the polymerase binds and thus initiates the transcription process. There are a variety of such promoters in use, which work with different efficiencies (strong and weak promoters). They are different for prokaryotic and eukaryotic cells.

The promoters that can be used in the present invention may be either constitutive, for example, the int promoter of bacteriophage Δ, the bla promoter of the β-lactamase gene of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene of pPR325, etc., or inducible, such as the prokaryotic promoters including the major right and left promoters of bacteriophage Δ (P_L and P_R),

the trp, recA, lacZ, lacI, ompF and gal promoters of E. coli, or the trp-lac hybrid promoter, etc. (Glick, B.R. (1987)). Besides the use of strong promoters to generate large quantities of mRNA, in order to achieve high levels of gene expression in prokaryotic cells, it is necessary to use also ribosome-binding sites to ensure that the mRNA is efficiently translated. One example is the Shine-Dalgarno sequence (SD sequence) appropriately positioned from the initiation codon and complementary to the 3'-terminal sequence of 16S RNA.

For eukaryotic hosts, different transcriptional and translational regulatory sequences bay be employed, depending on the nature of the host. They may be derived from viral sources, such as adenovirus, bovine papilloma virus, Simian virus, or the like, where the regulatory signals are associated with a particular gene which has a high level of expression. Examples are the TK promoter of Herpes virus, the SV40 early promoter, the yeast ga14 gene promoter, etc. Transcriptional initiation regulatory signals may be selected which allow for repression and activation, so that expression of the genes can be modulated.

The DNA molecule comprising the nucleotide sequence coding for the peptides or other molecules of the invention and the operably linked transcriptional and translational regulatory signals is inserted into a vector which is capable of integrating the desired gene sequences into the host cell chromosome. The cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotropic host, biocide resistance, e.g., antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of single chain binding protein mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama, H., (1983).

In a preferred embodiment, the introduced DNA molecule will be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector; the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in E. coli, for example, pBR322, ColEI, pSC101, pACYC 184, etc. (see Maniatis et al., (1982)); Bacillus plasmids such as pC194, pC221, pT127, etc. (Gryczan, T., (1982)-); Streptomyces plasmids including pIJ101 (Kendall, K.J. et al., (1987)); Streptomyces bacteriophages such as ØC31 (Chater, K.F. et al., in: Sixth International Symposium on Actinomycetales Biology, (1986)), and Pseudomonas plasmids (John, J.F., et al. (1986), and Izaki, K. (1978)). Preferred eukaryotic plasmids include BPV, vaccinia, SV40, 2-micron circle, etc., or their derivatives. Such plasmids are well known in the art (Botstein. D., et al. (1982); Broach, J.R., in: The Molecular Biology of the Yeast Saccharomyces: Life Cycle and Inheritance, (1981); Broach, J.R., (1982); Bollon, D.P., et al. (1980); Maniatis, T., in: Cell Biology: A Comprehensive Treatise, Vol. 3: Gene Expression, (1980)).

Once the vector or DNA sequence containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means: transformation, transfection, conjugation, protoplast fusion, electroporation, calcium phosphate-precipitation, direct microinjection, etc.

Host cells to be used in this invention may be either prokaryotic or eukaryotic. Preferred prokaryotic hosts include bacteria such as E. coli, Bacillus, Streptomyces, Pseudomonas, Salmonella, Serratia, etc. The most preferred prokaryotic host is E. coli. Bacterial hosts of particular interest include E. coli K12 strain 294 (ATCC 31446), E. coli X1776 (ATCC 31537), E. coli W3110 (F^-, $lambda^-$, prototropic (ATCC 27325)), and other enterobacterium such as Salmonella typhimurium or Serratia marcescens and various Pseudomonas species. Under such conditions, the protein will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

Preferred eukaryotic hosts are mammalian cells, e.g., human, monkey, mouse and chinese hamster ovary (CHO) cells, because they provide post-translational modifications to protein molecules including correct folding or glycosylation at correct sites. Also yeast cells can carry out post-translational peptide modifications including glycosylation. A number of recombinant DNA strategies exist which utilize strong promoter sequences and high copy number of plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian gene products and secretes peptides bearing leader sequences (i.e., pre-pep-

tides).

After the introduction of the vector, the host cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene sequence(s) results in the production of the desired proteins.

Purification of the recombinant proteins is carried out by any one of the methods known for this purpose.

Although reference is made throughout to the p55-TNF-R, it is evident from what is known of the p75-TNF-R, that it functions similarly. Therefore the present invention encompasses modulation of the signal transduction and/or cleavage in both known TNF receptors.

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Claims

1. A method of modulating signal transduction and/or cleavage in tumor necrosis factor receptors (TNF-Rs) comprising interfering with one or more amino acids in the sequence of a TNF-R or with an effector protein interacting with TNF-R.

2. The method according to claim 1, wherein the TNF-R is the human p55-TNF-R.

3. The method according to claim 1, wherein the TNF-R is the human p75-TNF-R.

4. A method for modulating signal transduction in TNF-Rs comprising interfering with amino acid(s) 405 to 415 or 197 ser of the human p55-TNF-R or the amino acids corresponding thereto in the human p75-TNF-R.

5. A method of inhibiting cleavage of the soluble form of the TNF-R comprising interfering with amino acid(s) 197 ser, 170-174, 175-179 or 170-179 of the human p55-TNF-R or the corresponding amino acid in the human p75-TNF-R.

6. A peptide or other molecule capable of interacting with either a TNF-R or an effector protein so as to modulate the normal functioning of the TNF-R.

7. The peptide or other molecule according to claim 6, capable of interacting with amino acid(s) 197 ser, 170-174, 170-179, 175-179 or 405-415 of the human p55-TNF-R or the corresponding amino acid in the human p75-TNF-R.

8. An effector protein capable of interacting with amino acid(s) 197 ser, 170-174, 170-179, 175-179 or 405-415 of the human p55-TNF-R or the corresponding amino acid in the human p75-TNF-R.

9. The effector protein according to claim 8, comprising a proteolytic enzyme.

10. An antibody capable of interacting with either a TNF-R or an effector protein so as to modulate the normal functioning of the TNF-R.

11. The antibody according to claim 10, capable of interacting with amino acid(s) 197 ser, 170-174, 170-179, 175-179 or 405-415 of the human p55-TNF-R or the corresponding amino acid in the human p75-TNF-R.

12. The antibody according to claim 10 or 11, being a monoclonal antibody.

13. A DNA molecule comprising the nucleotide sequence coding for a peptide or other molecule according to claim 6 or 7.

14. A replicable expression vehicle comprising the DNA molecule according to claim 13, capable, in a transformant host cell, of expressing the peptide or other molecule according to claim 6 or 7.

15. A host cell transformed with the replicable expression vehicle according to claim 14.

16. A pharmaceutical composition comprising as active ingredient a peptide or other molecule according to claim 6 or 7.

1 CGCCCCAGTCATCTTCA 17

18 ACGCCAAAGGCCAGAACTCCAGCCTCAGTCCACAGAATTCTGAGAAAATTAAAGCACAGAGCAGGGGACAGATCACTGGCACCAGCCCCTGATCTCTATGCCCCAGTCTCAACCCTCAA 136

137 CTGTCACCCCAAAGCCACTTGGGACGTCCTGGACAGACCGAGTCCCCGGAAGCCCCAGCACTGCGGCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCATAGCTGTCTGGC 255

-20 -10 -1 +1

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu

256 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG 345

10 20 30

Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr

346 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435

40 50 60

Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr

436 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC 525

70 80 90

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp

526 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC 615

100 110 120

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu

616 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC 705

130 140 150

Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val

706 AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC 795

160 Δ(170–174) Δ(170–179) Δ(175–179) 180

Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr

796 TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC 885

190 S197A 200 210

Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys

886 ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG 975

Δ(215–426) 220 230 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn

976 TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC 1065

Δ(244–426) 250 260 270

Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr

1066 CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC 1155

280 290 300

Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala

1156 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC 1245

Δ(310–426) 320 330

Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr

1246 TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC 1335

340 Δ(343–426) 350 360

Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu

1336 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG 1425

370 Δ(376–426) 380 390

Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu

1426 CAG AAC GGG CGC TGC CTG CGC GAG GCC CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG 1515

400 Δ(408–426) 410 Δ(413–426) 420

Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala

1516 CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG 1605

426

Pro Ser Leu Leu Arg End

1606 CCC AGT CTT CTC AGA TGA GGCTGCGCCCCTGCGGGCAGCTCTAAGGACCGTCCTGCGAGATCGCCTTCCAACCCCACTTTTTTCTGGAAAGGAGGGGTCCTGCAGGGGCAAGCA 1718

1719 GGAGCTAGCAGCCGCCTACTTGGTGCTAACCCCTCGATGTACATAGCTTTTCTCAGCTGCCTGCGCGCCGCCGACAGTCAGCGCTGTGCGCGCGGAGAGAGGTGCGCCGTGGGCTCAAG 1837

1838 AGCCTGAGTGGGTGGTTTGCGAGGATGAGGGACGCTATGCCTCATGCCCGTTTTGGGTGTCCTCACCAGCAAGGCTGCTCGGGGGCCCCTGGTTCGTCCCTGAGCCTTTTTCACAGTGC 1956

1957 ATAAGCAGTTTTTTTTGTTTTTGTTTTGTTTTGTTTTGTTTTTAAATCAATCATGTTACACTAATAGAAACTTGGCACTCCTGTGCCCTCTGCCTGGACAAGCACATAGCAAGCTGAAC 2075

2076 TGTCCTAAGGCAGGGGCGAGCACGGAACAATGGGGCCTTCAGCTGGAGCTGTGGACTTTTGTACATACACTAAAATTCTCAAGTTAAAAAAAAAAAAAA 2175

FIGURE 1

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Cytoplasmic deletion mutants of the p55 TNF-R

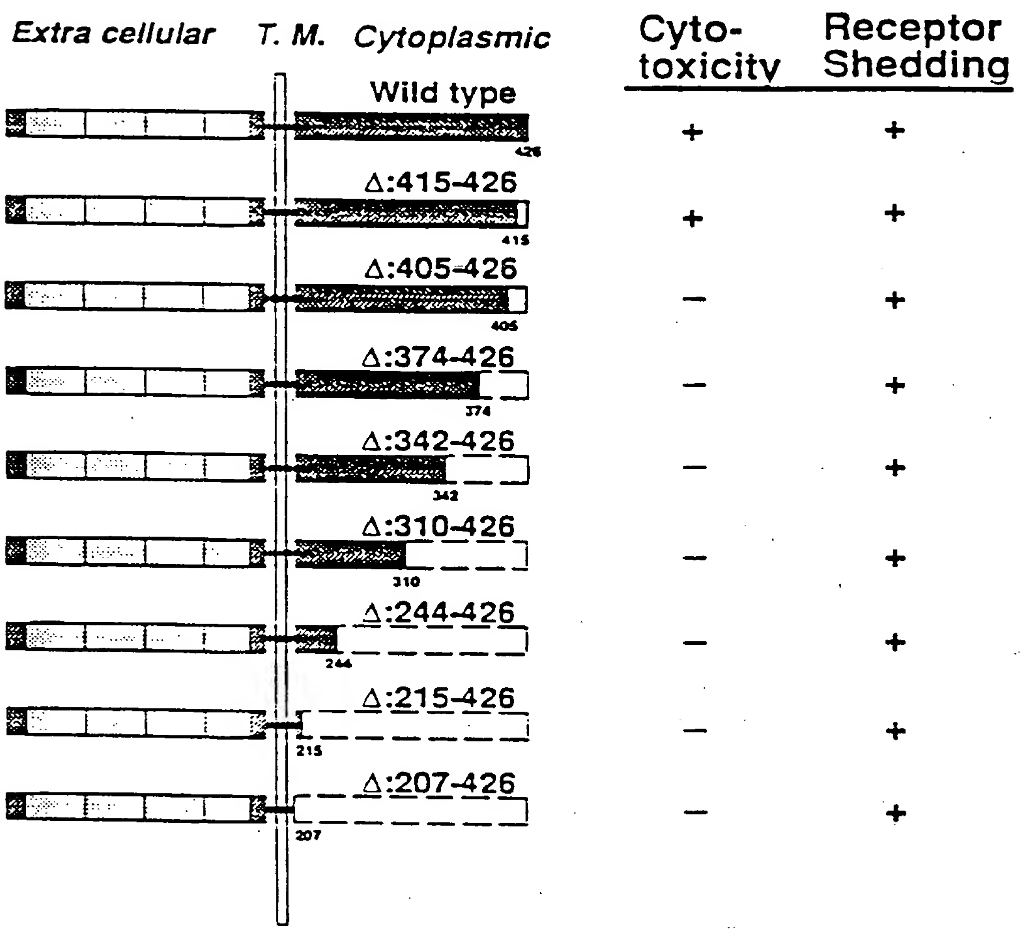

FIGURE 2

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The region 410-415, but not 415-426, in the intracellular domain of the p55 TNF-R plays a role in signalling

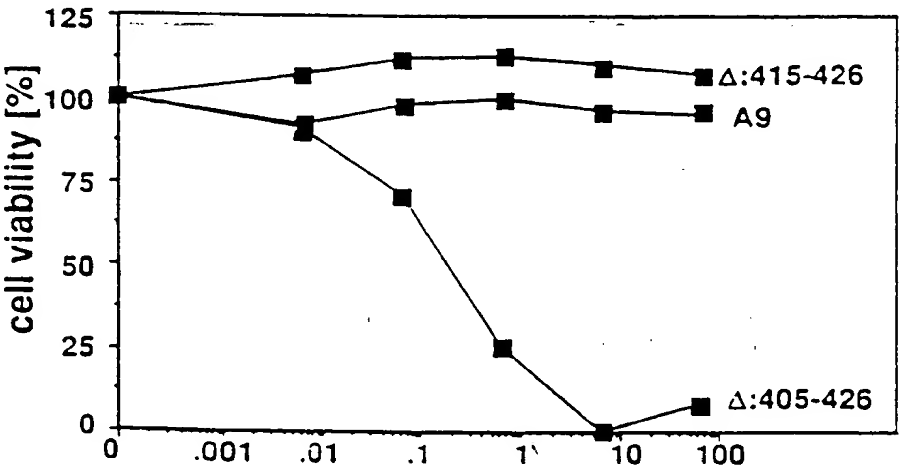

FIGURE 3

Exchange of serine in the transmembrane domain against alanine reduces the signalling for cell death

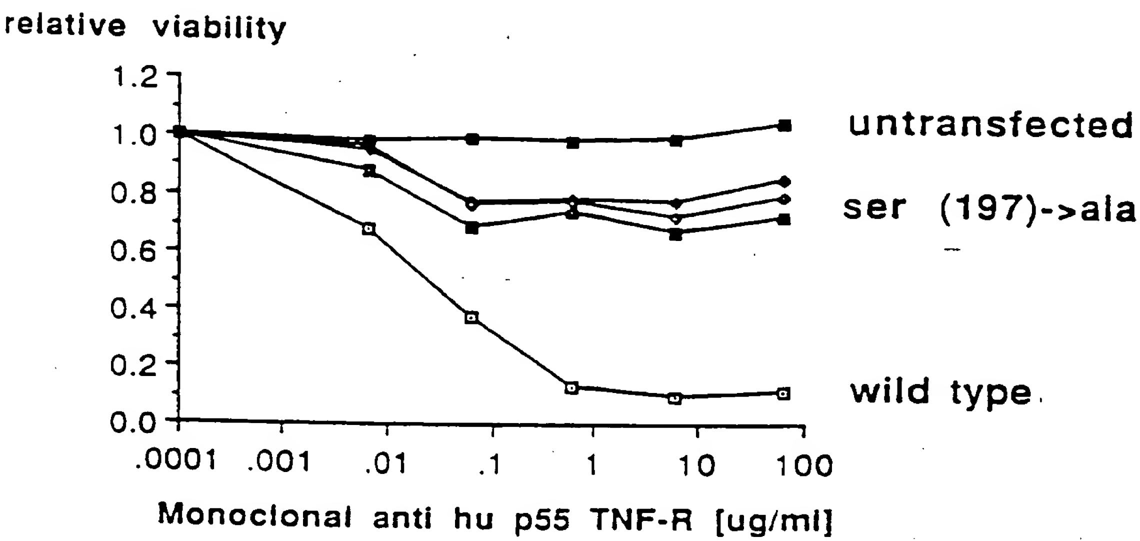

FIGURE 4

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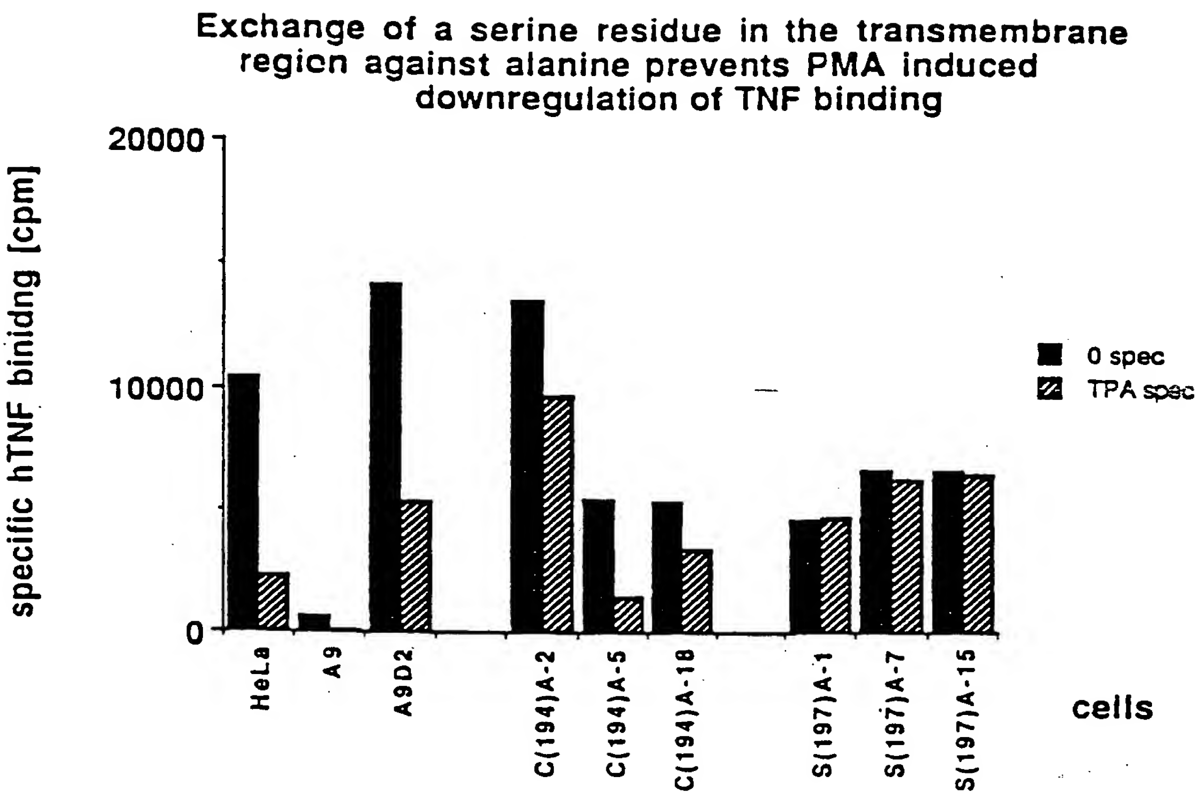
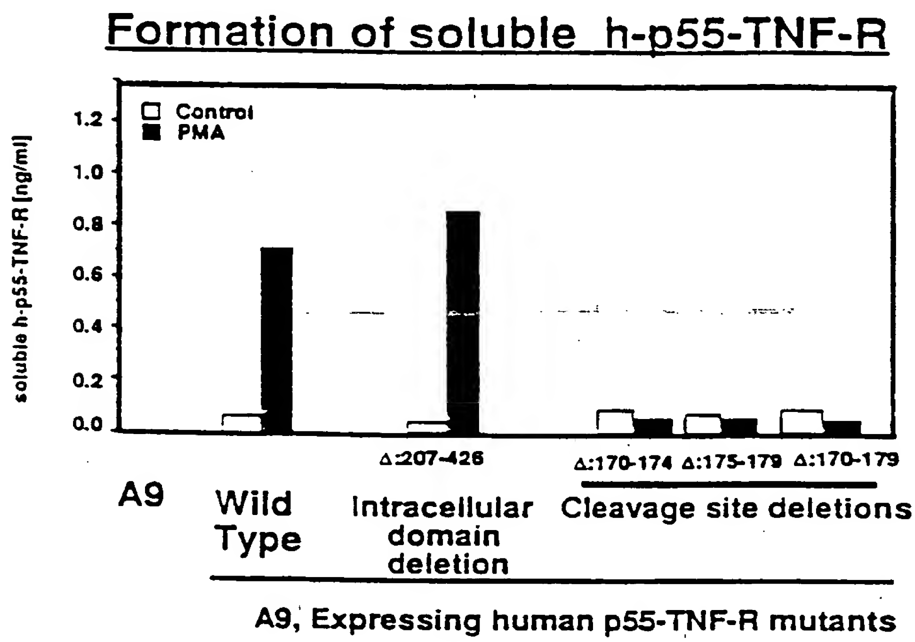


Exchange of a serine residue in the transmembrane region against alanine prevents PMA induced downregulation of TNF binding
specific hTNF binidng [cpm]
20000
10000
0
0 spec
TPA spec
HeLa
A9
A9D2
C(194)A-2
C(194)A-5
C(194)A-18
S(197)A-1
S(197)A-7
S(197)A-15
cells

FIGURE 5

EFFECT OF COMPLETE DELETION OF THE INTRACELLULAR DOMAIN AND OF DELETION OF THE PUTATIVE CLEAVAGE SITE, ON THE FORMATION OF THE SOLUBLE TNF-R



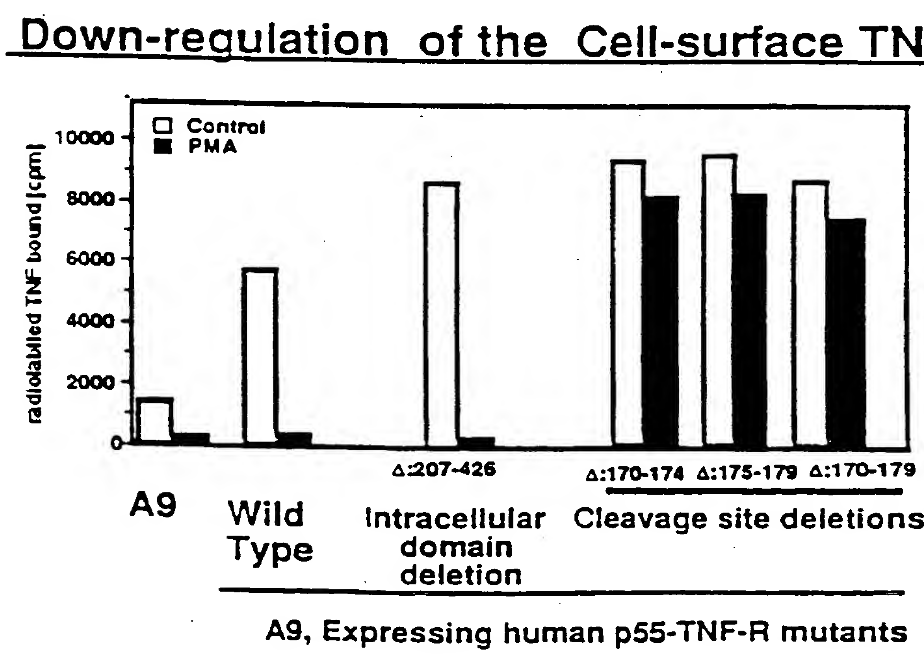


FIGURE 6